

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 28, 2002, 17:40:15 ; Search time 63.43 Seconds  
(without alignments)  
679.107 Million cell updates/sec

Title: US-09-502-984B-37  
Perfect score: 1284  
Sequence: 1 KFEKSKALLAARGPEELICF ..... RKNRELEEEVERLKLQVGER 249

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	903.5	70.4	509	6	Q9MYZ9 sus scrofa
2	888	69.2	316	11	Q35545 ratius norv
3	782	60.9	229	6	Q27950 bos indicus
4	778	60.6	229	6	Q28206 bos taurus
5	719.5	56.0	418	6	Q95N13 ovis aries
6	719.5	56.0	418	6	Q95N14 ovis aries
7	152	11.8	566	11	Q925F5 mus musculu
8	133.5	10.4	422	4	Q75462 homo sapien
9	132.5	10.3	422	4	Q9UHH5
10	128.5	10.0	425	11	Q9JMS8
11	118	9.2	296	6	Q18880 bos taurus
12	114.5	8.9	521	4	Q96TF0
13	112.5	8.8	581	6	Q46561 ovis aries
14	112.5	8.8	634	6	Q46600 bos taurus
15	111.5	8.7	626	13	Q90W67 cynops pyr
16	108	8.4	35	3	Q96UT3 saccharomyc

17	107	8.3	608	6	Q9N0Y7	Q9N0Y7 monodelphis
18	106.5	8.2	611	13	Q9PT89	Q9PT89 xenopus lae
19	105.5	8.2	638	6	Q95TF2	Q95TF2 aliuropoda
20	102.5	8.0	628	11	Q9JKT1	Q9JKT1 cavia porce
21	102.5	8.0	628	11	Q9JKT1	Q9JKT1 cavia porce
22	102.5	8.0	628	11	Q9JKT1	Q9JKT1 cavia porce
23	102	7.9	638	6	Q9U69	Q9U69 canis faml
24	101.5	7.9	848	6	Q9WZS2	Q9WZS2 sus scrofa
25	99.5	7.7	1165	6	Q9U69	Q9U69 sus scrofa
26	99.5	7.7	1469	5	Q9U190	Q9U190 sus scrofa
27	99	7.7	622	6	Q9N0J7	Q9N0J7 leishmania
28	99	7.7	894	6	Q9MYL1	Q9MYL1 callithrix
29	99	7.7	925	6	Q9MYK9	Q9MYK9 macaca mula
30	99	7.7	1163	6	Q9MYL2	Q9MYL2 macaca mula
31	99	7.7	1194	6	Q9MYT0	Q9MYT0 macaca mula
32	98.5	7.7	538	4	Q9HBE5	Q9HBE5 homo sapien
33	98.5	7.7	538	4	Q9HBE5	Q9HBE5 homo sapien
34	96.5	7.5	390	4	Q9U6H7	Q9U6H7 homo sapien
35	96.5	7.5	1093	11	Q70535	Q70535 ratius norv
36	96.5	7.5	1627	5	Q96200	Q96200 giardia lam
37	96	7.5	896	4	Q92919	Q92919 homo sapien
38	96	7.5	896	4	Q13594	Q13594 homo sapien
39	96	7.5	906	4	Q13593	Q13593 homo sapien
40	96	7.5	958	4	Q92920	Q92920 homo sapien
41	96	7.5	958	4	Q13592	Q13592 homo sapien
42	96	7.5	1165	4	Q92921	Q92921 homo sapien
43	95.5	7.4	611	13	Q91BF6	Q91BF6 xenopus lae
44	95.5	7.4	611	13	Q9PT10	Q9PT10 xenopus lae
45	95.5	7.4	636	13	Q90Z16	Q90Z16 paratichthy

## ALIGNMENTS

RESULT	ID	Q9MYZ9	PRELIMINARY:	PRT:	509 AA.
AC	Q9MYZ9;	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)				
DE	01-DEC-2001 (TREMBLrel. 19, last annotation update)				
DR	ERYTHROPOIETIN RECEPTOR.				
DS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
NCBI_Taxid=9823;					
RP	SEQUENCE FROM N.A.				
RC	TISSUE=LIVER;				
RA	Pearson P.L., Smith T.P.L., Sonstegard T.S., Klemcke H.G.,				
RT	Christenson R.K., Vallet J.L.,				
RT	"Porcine Erythropoietin Receptor: Molecular Cloning and Expression in				
RT	Domestic Anim. Endocrinol. 0:0-0(2000).				
DR	EMBL: AF274305; AAF77065.1; -				
DR	HSSP: P19235; 1EBA.				
DR	InterPro: IPR002996; CRA.				
DR	InterPro: IPR000572; Euk_Oxidored_molyb.				
DR	InterPro: IPR003961; FN_III.				
DR	InterPro: IPR003528; Hematopo_receptor_L_F1.				
DR	Pfam: PF00041; fn3; 1.				
DR	SMART: SM00060; FN3; 1.				
DR	PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.				
DR	PROSITE: PS00559; MOLYBDOPTERIN_EUK; UNKNOWN_1.				
KW	RECEPTOR.				
SEQUENCE	509 AA; 55183 MW; 35B565D07C6BCD8A CRC64;				

Query Match 70.4%; Score 903.5; DB 6; Length 509;  
Best Local Similarity 80.2%; Pred. No. 2.5e-71;  
Matches 170; Conservative 18; Mismatches 23; Indels 1; Gaps 1;  
QY 1 KFEKSKALLAARGPEELICFTEFLDLVCFEEAASAGVGNGFSFQLEDEPWKICRL 60

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Db      34  KFSKALLAARPEELCTERLEDLVCFWEAGSAGVPEDEYSFESYQLEGEPMKCHL 93
Qy      61  HQAPTARGAIRFCISLPTADTSSFFVLELRLT-AASGAPRHVHINEVLLDAPVGLV 119
Db      94  HQAPTARGAIRFCISLPTADTSSFFVLELRLVTEVSSGAPRHVHINEVLLDAPVGLL 153
Qy     120  ARLADESGHVIVRWLPPETPMTSHIRFELDLSAGNGAGSVORVELLEGTECVLSNLRG 179
Db     154  ARAEESGHVILRWLPPPGAPMASLIRVENVISTENAGAGVQREVLIDGRTECVLSNLRG 213
Qy     180  RRTITAVRARMAEPSFGFMSAMSEPVSLT 211
Db     214  GTRYTFVRRARMAEPSFGFMSAMSEPVSLT 245

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RESULT 2
035545 PRELIMINARY; PRT; 316 AA.
ID 035545;
AC 035545;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTRON 5-INSERTED FORM OF ERYTHROPOIETIN RECEPTOR PRECURSOR.
OS Rattus norvegicus (Rat).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDJINE-9829611; PubMed-9630610;
RA Yamae J. R., Murakami C., Takenoshita M., Tsuyama S., Inui H.,
RA Miyake K., Nakano Y.;
RT "The intron 5-inserted form of rat erythropoietin receptor is
RT expressed as a membrane-bound form."
RL Biochim. Biophys. Acta 1403:169-178 (1998).
DR EMBL; D83509; BAA22373.1; -.
DR HSSP; P19235; IEBA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hematopo_receptor_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; fn3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW Signal; Receptor.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 316 POTENTIAL.
SQ SEQUENCE 316 AA; 34220 MW; 05C44BF8516C180B CRC64;

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Query Match 69.2%; Score 888; DB 11; Length 316;  
 Best Local Similarity 75.1%; Pred. No. 3.2e-70;  
 Matches 169; Conservative 24; Mismatches 22; Indels 10; Gaps 2;

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Qy      1  KESKALLAARPEELCTERLEDLVCFEEAASAGVPRGPFSPFQLEDEPMKCLR 60
Db     34  KFSKALLAARPEELCTERLEDLVCFWEAASAGV-FVYSPSYQLEGSRRSCL 92
Qy     61  HQAPTARGAIRFCISLPTADTSSFFVLELRLTAASGAPRHVHINEVLLDAPVGLV 120
Db     93  HQAPTARGAIRFCISLPTADTSSFFVLELRLVTEVSSGAPRHVHINEVLLDAPVGLL 152
Qy    121  RLADESGHVIVRWLPPETPMTSHIRFELDLSAGNGAGSVORVELLEGTECVLSNLGR 180
Db    153  RRAEESGHVILRWLPPPGAPMASLIRVENVISTENAGAGVQREVLIDGRTECVLSNLRG 212
Qy    181  RRTITAVRARMAEPSFGFMSAMSEPVSLT-----GGGS 216
Db    213  TRYTFVRRARMAEPSFGFMSAMSEPVSLTASGEATVPRGGGA 257

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RESULT 3
027950

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ID 027950 PRELIMINARY; PRT; 229 AA.
AC 027950;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ERYTHROPOIETIN RECEPTOR (FRAGMENT).
GN EFOR.
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-BONE MARROW;
RA Suliman H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U61398; AAB03870.1; -.
DR HSSP; P19235; IEBA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hematopo_receptor_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; fn3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 229 229
SQ SEQUENCE 229 AA; 25196 MW; F6E01C4AB07893E8 CRC64;

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Query Match 60.9%; Score 782; DB 6; Length 229;  
 Best Local Similarity 78.5%; Pred. No. 4.6e-61;  
 Matches 146; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

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Qy     26  DLVCFEEAASAGVPRGPFSPFQLEDEPMKCLRHOAPTARGAIRFCISLPTADTSSFFV 85
Db     1  DLVCFWEAATAGVPRGPNNSFESYQLEGEPMKPCRLHOAPTARGLVPRWCSLPTADTSSFFV 60
Qy     86  PLELRRLTAASGAPRHVHINEVLLDAPVGLVARLADESGHVIVRWLPPETPMTSHI 145
Db     61  PLELHTTAASGASRRYRTHVNEVLLDPPARLVARRADSGHVIVRWLPPPGAPMASLI 120
Qy    146  RFLDLSAGNGAGSVORVELLEGTECVLSNLGRRTITAVRARMAEPSFGFMSAMSE 205
Db    121  RVEVNVISAENAAAGSAQREVLIDGRTECVLSNLGRGTRYTFVRRARMAEPSFGFMSAMSE 180
Qy    206  PVSLLT 211
Db    181  PASLLT 186

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RESULT 4
028206 PRELIMINARY; PRT; 229 AA.
ID 028206;
AC 028206;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ERYTHROPOIETIN RECEPTOR (FRAGMENT).
GN EFOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-BONE MARROW;
RA Suliman H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U61399; AAB03871.1; -.
DR HSSP; P19235; IEBA.

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Query Match	56.0%;	Score 719.5;	DB 6;	Length 387;
Best Local Similarity	76.4%;	Pred. No. 2.8e-55;		
Matches 136;	Conservative 14;	Mismatches 27;	Indels 1;	Gaps 1;
OY	35	ASAAVGPGNFSFQQLDEDEPWKICLTHQAPPARAGAIIFWCSLPTADTSSFVLELRITAA	94	
		:       :                   :		
Db	3	ATAAGVPGPNYSFSYQLEGEPPWKPCRLHOTPTARGIVRFWCSLPTADTSSFVLELRITAA	62	
OY	95	- SGAPREHRYHINENVLLDAPVGLVARLADSGHVVIRLWLPPEPTPKMISHIRFELDISA	153	
		:     :     :     :     :     :     :     :     :     :     :		
Db	63	SSGASRYRRTIRHVENVLLDPPARIVARRADEGGHVVIRLWLPPEAPAMSLIRYEYNISA	122	
OY	154	GNAGASVQVRELLGREGCEVLNLNGRRIRITIAVARAAEPSEFGFGWAMSEPVSLIT	211	
		:       :		

Query Match	11.88;	Score 152;	DB 11;	Length 566;
Best Local Similarity	24.98;	Pred. No. 4,1e-05;		
Matches 55;	Conservative 28;	Mismatches 96;	Indels 42;	Gaps 8;

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Db 18 SDOVFLLATGTEPLNCFSSQFFEDLTCFWEDEEA--PSGTYOLLYVYRGKPRACPLYSQ 75
OY 64 PTARGAIREWCSLPTADTSSFPLELRLTAAS--GAPRFH-RVHINEVLLDAPVG 117
Db 76 SVTFEGTRIVCOPPADDEVLEFFPLHVMKNVSLNOTLIORVLFVDSVETCCPTLMNP 135
OY 109 VLLDAPVGLVARLADESGHVIRMLPPETPMTSHIRFELDISAGNGAGSVORVELLEG 168
Db 136 VPVLDDP-PCVHPPTASOP--HGVPRTSPAGAPF-----LTVKGS----- 173
OY 169 RTCEVLSNRGRTITIAVARARAEPSPFGFSWAMSEPVSL 209
Db 174 ---CLVSGLOAGRSYWLQKSPDQVSLRSGWSPSPVTV 211

RESULT 8
ID 075462 PRELIMINARY; PRT: 422 AA.
AC 075462;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE CYTOKINE-LIKE FACTOR-1 PRECURSOR.
GN CLF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Elson G.C.A., Graber P., Losberger P., Herren S., Gretener D.,
RA Menoud L.N., Wells T.N.C., Kosco-Villbois M.H., Gauchat J.F.;
RT "CLF-1, a Novel Soluble Protein Shares Homology With Members of the
RT Cytokine Type-1 Receptor Family.";
RL J. Immunol. 0:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Magrangas F., Jacques Y., Minville S.;
RT "Cloning and expression of a novel soluble protein containing
RT hematopoietic cytokine receptor domains.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF059293; AAC28335.1; -;
DR EMBL: AF073515; AAD39681.1; -;
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR Pfam: PR00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
KW Signal; Receptor.
FT SIGNAL. 1 37
FT CHAIN 38 422 CYTOKINE-LIKE FACTOR-1.
SQ SEQUENCE 422 AA; 46301 MW; AD9DEFB01B8428 CRC64;

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Query Match 10.4%; Score 133.5; DB 4; Length 422;  
 Best Local Similarity 23.7%; Pred. No. 0.0012;  
 Matches 64; Conservative 37; Mismatches 98; Indels 71; Gaps 16;

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OY 14 PELLCTERLELDVCFEEFAASAGVPG-----NFSFQLEDEPW---KICRL 60
Db 138 PVNISCMKMKKDLTCRWT-----PGAHGTFPLHTNLSLYKLR--WYGDMTCCE 186
OY 61 HQAPTARGAIREWCSLPTADTSSFPLELRLTAAS--GAPRFH-RVHINEVLLDAPVG 117
Db 187 YHIVGHS-----CHIP-KDLAFTPEIWEATNRLGSAKSVLLDILDVYTTDPPPD 240
OY 118 L-VARLADESGHVIRMLPPET-----PMTSHIRFELDISAGNGAGSVORVELLEG 171
Db 241 VHSVRVGGLEDQLSVRVSPALKDPLFOAKYQIRYVEDSV-----DMKVVDVSNQTS 295
OY 172 CVLSNLRGRTITIAVARARAEPSPFG-----GFSWAMSEPVSLT-----GGGGRM 218

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Db 296 CRLAGLKPGTVIVVOYRCN----PFGIYSKKAGINSEMSHPAASPSEPPGCGGAC 351
OY 219 EKLEOKVKELLRKNERLEEVEER-LKQLVG 247
Db 352 EP-----RGEPSSGPRRELKQFLG 372

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RESULT 9
ID 090HH5 PRELIMINARY; PRT: 422 AA.
AC 090HH5;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE CLASS I CYTOKINE RECEPTOR.
GN ZCYTOR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lok S., Presnell S.R., Jelmberg A.C., Gilbert T., Whitmore T.E.,
RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF178684; AAD54385.1; -;
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR Pfam: PR00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
KW Receptor.
SQ SEQUENCE 422 AA; 46315 MW; 0D2C5F7A01B942EE CRC64;

```

Query Match 10.3%; Score 132.5; DB 4; Length 422;  
 Best Local Similarity 23.7%; Pred. No. 0.0015;  
 Matches 64; Conservative 37; Mismatches 98; Indels 71; Gaps 16;

```

OY 14 PELLCTERLELDVCFEEFAASAGVPG-----NFSFQLEDEPW---KICRL 60
Db 138 PVNISCMKMKKDLTCRWT-----PGAHGTFPLHTNLSLYKLR--WYGDMTCCE 186
OY 61 HQAPTARGAIREWCSLPTADTSSFPLELRLTAAS--GAPRFH-RVHINEVLLDAPVG 117
Db 187 YHIVGHS-----CHIP-KDLAFTPEIWEATNRLGSAKSVLLDILDVYTTDPPPD 240
OY 118 L-VARLADESGHVIRMLPPET-----PMTSHIRFELDISAGNGAGSVORVELLEG 171
Db 241 VHSVRVGGLEDQLSVRVSPALKDPLFOAKYQIRYVEDSV-----DMKVVDVSNQTS 295
OY 172 CVLSNLRGRTITIAVARARAEPSPFG-----GFSWAMSEPVSLT-----GGGGRM 218
Db 296 CRLAGLKPGTVIVVOYRCN----PFGIYSKKAGINSEMSHPAASPSEPPGCGGAC 351
OY 219 EKLEOKVKELLRKNERLEEVEER-LKQLVG 247
Db 352 EP-----RGEPSSGPRRELKQFLG 372

RESULT 10
ID 09JMS8 PRELIMINARY; PRT: 425 AA.
AC 09JMS8;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE CYTOKINE RECEPTOR LIKE MOLECULE 3 PRECURSOR.
GN CR1F1 OR CR1M3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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